



SEQUENCE LISTING

<11> RASTELLI, LUCA

<120> NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING
SAME

<130> 10716-08

<140> 09/784,810

<141> 2001-02-14

<150> 60/182,360

<151> 2000-02-14

<150> 60/191,261

<151> 2000-03-22

<160> 29

<170> PatentIn Ver. 2.1

<210> 1

<211> 1600

<212> DNA

<213> Homo sapiens

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<223> a, t, c, g, other or unknown

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 <211> 384
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Phe Thr Leu Met Leu Thr Glu Arg Arg Asn His Ala Arg Glu Leu Val
 50 55 60
 Arg Ser Glu Glu Leu Gly Arg Trp Asp Ala Leu Val Val Met Ser Gly
 65 70 75 80
 Asp Gly Leu Met His Glu Val Val Asn Gly Leu Met Glu Arg Pro Asp
 85 90 95
 Trp Glu Thr Ala Ile Gln Lys Pro Leu Cys Ser Leu Pro Ala Gly Ser
 100 105 110
 Gly Asn Ala Leu Ala Ala Ser Leu Asn His Tyr Ala Gly Tyr Glu Gln
 115 120 125
 Val Thr Asn Glu Asp Leu Leu Thr Asn Cys Thr Leu Leu Leu Cys Arg
 130 135 140
 Pro Val Leu Ser Pro Met Asn Leu Leu Ser Leu His Thr Ala Ser Gly
 145 150 155 160
 Leu Arg Ser Phe Ser Val Leu Ser Leu Ala Trp Gly Phe Ile Ala Asp
 165 170 175
 Val Asp Leu Glu Ser Asp Lys Tyr Arg Arg Leu Gly Glu Met Arg Phe
 180 185 190
 Thr Leu Gly Thr Phe Leu Arg Leu Ala Ala Leu Arg Thr Tyr Arg Gly
 195 200 205
 Arg Leu Ala Thr Leu Pro Val Gly Arg Val Gly Phe Lys Thr Pro Ala
 210 215 220
 Ser Pro Val Val Val Gln Gln Gly Pro Val Asp Ala His Leu Val Pro
 225 230 235 240
 Leu Glu Glu Gln Val Pro Ser His Trp Gln Val Val Pro Asp Glu Asp
 245 250 255

Phe Val Leu Val Leu Ala Leu Leu His Ser His Leu Ala Ser Glu Met
260 265 270

Phe Ala Ala Pro Met Gly Arg Cys Ala Ala Gly Val Met His Leu Phe
275 280 285

Tyr Val Arg Ala Gly Val Ser Arg Ala Met Leu Leu Arg Leu Phe Leu
290 295 300

Ala Met Glu Lys Gly Arg His Met Glu Tyr Glu Cys Pro Tyr Leu Val
305 310 315 320

Tyr Val Pro Val Val Ala Phe Arg Leu Glu Pro Lys Asp Gly Lys Gly
325 330 335

Val Phe Ala Val Asp Gly Glu Leu Met Val Ser Glu Ala Val Gln Gly
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Gln Val His Pro Asn Tyr Phe Trp Met Val Ser Gly Cys Val Glu Pro
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Pro Pro Ser Trp Lys Pro Gln Gln Met Pro Pro Pro Glu Glu Pro Leu
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<210> 3

<211> 1759

<212> DNA

<213> Mus musculus

<400> 3

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aagacctgct catcaactgc aactgctgt tgtgccgccg gcgcctgtca cccatgaacc 780
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<210> 4

<211> 382

<212> PRT

<213> Mus musculus

<400> 4

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      20              25              30

Leu Phe Gln Ser Arg Val Gln Pro Phe Leu Glu Glu Ala Glu Ile Thr
      35              40              45

Phe Lys Leu Ile Leu Thr Glu Arg Lys Asn His Ala Arg Glu Leu Val
      50              55              60

Cys Ala Glu Glu Leu Gly His Trp Asp Ala Leu Ala Val Met Ser Gly
      65              70              75              80

Asp Gly Leu Met His Glu Val Val Asn Gly Leu Met Glu Arg Pro Asp
      85              90              95

Trp Glu Thr Ala Ile Gln Lys Pro Leu Cys Ser Leu Pro Gly Gly Ser
      100             105             110

Gly Asn Ala Leu Ala Ala Ser Val Asn His Tyr Ala Gly Tyr Glu Gln
      115             120             125

Val Thr Asn Glu Asp Leu Leu Ile Asn Cys Thr Leu Leu Leu Cys Arg
      130             135             140

Arg Arg Leu Ser Pro Met Asn Leu Leu Ser Leu His Thr Ala Ser Gly
      145             150             155             160

Leu Arg Leu Tyr Ser Val Leu Ser Leu Ser Trp Gly Phe Val Ala Asp
      165             170             175

Val Asp Leu Glu Ser Glu Lys Tyr Arg Arg Leu Gly Glu Ile Arg Phe
      180             185             190

Thr Val Gly Thr Phe Phe Arg Leu Ala Ser Leu Arg Ile Tyr Gln Gly
      195             200             205

Gln Leu Ala Tyr Leu Pro Val Gly Thr Val Ala Ser Lys Arg Pro Ala
      210             215             220

Ser Thr Leu Val Gln Lys Gly Pro Val Asp Thr His Leu Val Pro Leu
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<210> 5
<211> 1840
<212> DNA
<213> Homo sapiens
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tacgctttta	cagttcactg	tgtaaagaga	gcacgacggc	accgctggaa	gtgggcgcag	180
gtgactttct	ggtgtccaga	ggagcagctg	tgtcacttgt	ggctgcagac	cctgcgggag	240
atgctggaga	agctgacgtc	cacagcaaag	catcttactgg	tatttatcaa	cccgtttgga	300
ggaaaaggac	aaggcaagcg	gatatatgaa	agaaaagtgg	caccactgtt	caccttagcc	360
tcocatcacca	ctgacatcat	cggtaacaaa	ttctatgtta	actatgtaga	agtaattact	420
gaacatgcta	atcaggccaa	ggagactctg	tatgagatta	acatagacaa	atacgacggc	480
atcgtctgtg	tcggcgggaga	tggtatgttc	agcgaggtgc	tgcacggtct	gattgggagg	540
acgcagagga	gcgcgggggt	cgaccagaac	cacccccggg	ctgtgctggg	ccccagtagc	600
ctccggattg	gaatcattcc	cgcagggtca	acggactgcg	tgtgttactc	caccgtgggc	660
accagcgacg	cagaaacctc	ggcgctgcat	atcgttgttg	gggactcgct	ggccatggat	720
gtgtcctcag	tcaccacaa	cagcacactc	cttcgctact	ccgtgtccct	gctggggctac	780
ggctttctacg	gggacatcat	caaggacagt	gagaaagaac	ggtgggtggg	tcttgccaga	840
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ttcctccctg	cacaacacac	ggtgggatct	ccaagggata	ggaagccctg	ccgggcagga	960
tgctttgttt	gcaggcaaag	caagcagcag	ctggaggagg	agcagaagaa	agcactgtat	1020
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atcaatgccca	caaacatgtc	ctgtgcttgt	cgccggagcc	ccaggggcct	ctccccggct	1140
gcccacttgg	gagacgggtc	ttctgacctc	atcctcatcc	ggaaatgctc	caggttcaat	1200
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gagcttaacg	agggggggaa	gaagcgtttt	gggcacattt	gcagcagcca	cccctcctgc	1380
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aaaactatatt aagataatta ttacagacca attatgttga tatatacatt taaatgtaga 1620
aatttatattt tgatagttaa atcttgattt tagaagaaaa cccttttgtc aacaattttg 1680
tgtacatatt tggcattttc agttctgtac gcatctgcgg gttgcagccc acgccgctta 1740
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<210> 6

<211> 471

<212> PRT

<213> Homo sapiens

<400> 6

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          20              25              30

Gln Leu Cys His Leu Trp Leu Gln Thr Leu Arg Glu Met Leu Glu Lys
          35              40              45

Leu Thr Ser Arg Pro Lys His Leu Leu Val Phe Ile Asn Pro Phe Gly
          50              55              60

Gly Lys Gly Gln Gly Lys Arg Ile Tyr Glu Arg Lys Val Ala Pro Leu
          65              70              75              80

Phe Thr Leu Ala Ser Ile Thr Thr Asp Ile Ile Gly Asn Lys Phe Tyr
          85              90              95

Val Asn Tyr Val Glu Val Ile Thr Glu His Ala Asn Gln Ala Lys Glu
          100             105             110

Thr Leu Tyr Glu Ile Asn Ile Asp Lys Tyr Asp Gly Ile Val Cys Val
          115             120             125

Gly Gly Asp Gly Met Phe Ser Glu Val Leu His Gly Leu Ile Gly Arg
          130             135             140

Thr Gln Arg Ser Ala Gly Val Asp Gln Asn His Pro Arg Ala Val Leu
          145             150             155             160

Val Pro Ser Ser Leu Arg Ile Gly Ile Ile Pro Ala Gly Ser Thr Asp
          165             170             175

Cys Val Cys Tyr Ser Thr Val Gly Thr Ser Asp Ala Glu Thr Ser Ala
          180             185             190

Leu His Ile Val Val Gly Asp Ser Leu Ala Met Asp Val Ser Ser Val
          195             200             205

His His Asn Ser Thr Leu Leu Arg Tyr Ser Val Ser Leu Leu Gly Tyr
          210             215             220

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Gly Phe Tyr Gly Asp Ile Ile Lys Asp Ser Glu Lys Lys Arg Trp Leu
 225 230 235 240
 Gly Leu Ala Arg Tyr Asp Phe Ser Gly Leu Lys Thr Phe Leu Ser His
 245 250 255
 His Cys Tyr Glu Gly Thr Val Ser Phe Leu Pro Ala Gln His Thr Val
 260 265 270
 Gly Ser Pro Arg Asp Arg Lys Pro Cys Arg Ala Gly Cys Phe Val Cys
 275 280 285
 Arg Gln Ser Lys Gln Gln Leu Glu Glu Glu Gln Lys Lys Ala Leu Tyr
 290 295 300
 Gly Leu Glu Ala Ala Glu Asp Val Glu Glu Trp Gln Val Val Cys Gly
 305 310 315 320
 Lys Phe Leu Ala Ile Asn Ala Thr Asn Met Ser Cys Ala Cys Arg Arg
 325 330 335
 Ser Pro Arg Gly Leu Ser Pro Ala Ala His Leu Gly Asp Gly Ser Ser
 340 345 350
 Asp Leu Ile Leu Ile Arg Lys Cys Ser Arg Phe Asn Phe Leu Arg Phe
 355 360 365
 Leu Ile Arg His Thr Asn Gln Gln Asp Gln Phe Asp Phe Thr Phe Val
 370 375 380
 Glu Val Tyr Arg Val Lys Lys Phe Gln Phe Thr Ser Lys His Met Glu
 385 390 395 400
 Asp Glu Asp Ser Asp Leu Lys Glu Gly Gly Lys Lys Arg Phe Gly His
 405 410 415
 Ile Cys Ser Ser His Pro Ser Cys Cys Cys Thr Val Ser Asn Ser Ser
 420 425 430
 Trp Asn Cys Asp Gly Glu Val Leu His Ser Pro Ala Ile Glu Val Arg
 435 440 445
 Val His Cys Gln Leu Val Arg Leu Phe Ala Arg Gly Ile Glu Glu Asn
 450 455 460
 Pro Lys Pro Asp Ser His Ser
 465 470

<210> 7

<211> 522

<212> DNA

<213> Rattus sp.

<400> 7

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 cgcaccagct ggcagtggac cctgacctca atggcagggc tgtgcaggac ttccccatca 180

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gtgaactgga atttcttgac tcgataaact tcaacgaaag tgaagccaaa ctgatcctcc 360
tggttggtgt gccggatgag gaatctcagg aagttgaacc tggagcattt ccggataagg 420
atgaggtcag aagaccatc tcccagatgg gcaaattggg acaggccccc agggctccgg 480
ggacaagcac aggacatgtt ggtggagttg atagccagga ac 522

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<210> 8
 <211> 144
 <212> PRT
 <213> Rattus sp.

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<400> 8
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Pro Gly Gly Leu Ser Pro Phe Ala His Leu Gly Asp Gly Ser Ser Asp
          20              25              30

Leu Ile Leu Ile Arg Lys Cys Ser Arg Phe Asn Phe Leu Arg Phe Leu
      35              40              45

Ile Arg His Thr Asn Gln Glu Asp Gln Phe Gly Phe Thr Phe Val Glu
      50              55              60

Val Tyr Arg Val Lys Lys Phe Gln Phe Thr Ser Lys His Val Glu Asp
      65              70              75              80

Asp Asp Asn Asp Leu Lys Glu Leu Glu Lys Gln Lys Phe Gly Gln Ile
          85              90              95

Cys Lys Asp Asn Pro Pro Cys Ala Cys Pro Thr Ser Arg Ser Ser Trp
          100              105              110

Asn Cys Asp Gly Glu Val Leu His Ser Pro Ala Ile Glu Val Arg Val
      115              120              125

His Cys Gln Leu Val Arg Leu Phe Ala Arg Gly Ile Glu Glu Glu Ser
      130              135              140

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<210> 9
 <211> 382
 <212> DNA
 <213> Mus musculus

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tttgataggt aaatcttggt tt 382

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<210> 10
 <211> 79
 <212> PRT
 <213> Mus musculus

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 35 40 45
 Cys Asp Gly Glu Val Met His Ser Pro Ala Ile Glu Val Arg Val His
 50 55 60
 Cys Gln Leu Val Arg Leu Phe Ala Arg Gly Ile Glu Glu Glu Ser
 65 70 75

<210> 11
 <211> 326
 <212> PRT
 <213> Homo sapiens

<400> 11
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 20 25 30
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 35 40 45
 Glu Val Ile Thr Glu His Ala Asn Gln Ala Lys Glu Thr Leu Tyr Glu
 50 55 60
 Ile Asn Ile Asp Lys Tyr Asp Gly Ile Val Cys Val Gly Gly Asp Gly
 65 70 75 80
 Met Phe Ser Glu Val Leu His Gly Leu Ile Gly Arg Thr Gln Arg Ser
 85 90 95
 Ala Gly Val Asp Gln Asn His Pro Arg Ala Val Leu Val Pro Ser Ser
 100 105 110
 Leu Arg Ile Gly Ile Ile Pro Ala Gly Ser Thr Asp Cys Val Cys Tyr
 115 120 125
 Ser Thr Val Gly Thr Ser Asp Ala Glu Thr Ser Ala Leu His Ile Val
 130 135 140
 Val Gly Asp Ser Leu Ala Met Asp Val Ser Ser Val His His Asn Ser
 145 150 155 160

Thr Leu Leu Arg Tyr Ser Val Ser Leu Leu Gly Tyr Gly Phe Tyr Gly
 165 170 175
 Asp Ile Ile Lys Asp Ser Glu Lys Lys Arg Trp Leu Gly Leu Ala Arg
 180 185 190
 Tyr Asp Phe Ser Gly Leu Lys Thr Phe Leu Ser His His Cys Tyr Glu
 195 200 205
 Gly Thr Val Ser Phe Leu Pro Ala Gln His Thr Val Gly Ser Pro Arg
 210 215 220
 Asp Arg Lys Pro Cys Arg Ala Gly Cys Phe Val Cys Arg Gln Ser Lys
 225 230 235 240
 Gln Gln Leu Glu Glu Glu Gln Lys Lys Ala Leu Tyr Gly Leu Glu Ala
 245 250 255
 Ala Glu Asp Val Glu Glu Trp Gln Val Val Cys Gly Lys Phe Leu Ala
 260 265 270
 Ile Asn Ala Thr Asn Met Ser Cys Ala Cys Arg Arg Ser Pro Arg Gly
 275 280 285
 Leu Ser Pro Ala Ala His Leu Gly Asp Gly Ser Ser Asp Leu Ile Leu
 290 295 300
 Ile Arg Lys Cys Ser Arg Phe Asn Phe Leu Arg Phe Leu Ile Arg His
 305 310 315 320
 Thr Asn Gln Gln Asp Gln
 325

<210> 12
 <211> 453
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 12

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 35 40 45
 Lys Ala Lys Lys Leu Phe Met Thr Lys Ala Lys Pro Leu Leu Leu Ala
 50 55 60
 Ser Arg Cys Ser Ile Glu Val Val Tyr Thr Lys Tyr Pro Gly His Ala
 65 70 75 80
 Ile Glu Ile Ala Arg Glu Met Asp Ile Asp Lys Tyr Asp Thr Ile Ala
 85 90 95

Cys	Ala	Ser	Gly	Asp	Gly	Ile	Pro	His	Glu	Val	Ile	Asn	Gly	Leu	Tyr	100	105	110
Gln	Arg	Pro	Asp	His	Val	Lys	Ala	Phe	Asn	Asn	Ile	Ala	Ile	Thr	Glu	115	120	125
Ile	Pro	Cys	Gly	Ser	Gly	Asn	Ala	Met	Ser	Val	Ser	Cys	His	Trp	Thr	130	135	140
Asn	Asn	Pro	Ser	Tyr	Ser	Thr	Leu	Cys	Leu	Ile	Lys	Ser	Ile	Glu	Thr	145	150	155
Arg	Ile	Asp	Leu	Met	Cys	Cys	Ser	Gln	Pro	Ser	Tyr	Ala	Arg	Glu	His	165	170	175
Pro	Lys	Leu	Ser	Phe	Leu	Ser	Gln	Thr	Tyr	Gly	Leu	Ile	Ala	Glu	Thr	180	185	190
Asp	Ile	Asn	Thr	Glu	Phe	Ile	Arg	Trp	Met	Gly	Pro	Ala	Arg	Phe	Glu	195	200	205
Leu	Gly	Val	Ala	Phe	Asn	Ile	Ile	Gln	Lys	Lys	Lys	Tyr	Pro	Cys	Glu	210	215	220
Ile	Tyr	Val	Lys	Tyr	Ala	Ala	Lys	Ser	Lys	Asn	Glu	Leu	Lys	Asn	His	225	230	235
Tyr	Leu	Glu	His	Lys	Asn	Lys	Gly	Ser	Leu	Glu	Phe	Gln	His	Ile	Thr	245	250	255
Met	Asn	Lys	Asp	Asn	Glu	Asp	Cys	Asp	Asn	Tyr	Asn	Tyr	Glu	Asn	Glu	260	265	270
Tyr	Glu	Thr	Glu	Asn	Glu	Asp	Glu	Asp	Glu	Asp	Ala	Asp	Ala	Asp	Asp	275	280	285
Glu	Asp	Ser	His	Leu	Ile	Ser	Arg	Asp	Leu	Ala	Asp	Ser	Ser	Ala	Asp	290	295	300
Gln	Ile	Lys	Glu	Glu	Asp	Phe	Lys	Ile	Lys	Tyr	Pro	Leu	Asp	Glu	Gly	305	310	315
Ile	Pro	Ser	Asp	Trp	Glu	Arg	Leu	Asp	Pro	Asn	Ile	Ser	Asn	Asn	Leu	325	330	335
Gly	Ile	Phe	Tyr	Thr	Gly	Lys	Met	Pro	Tyr	Val	Ala	Ala	Asp	Thr	Lys	340	345	350
Phe	Phe	Pro	Ala	Ala	Leu	Pro	Ser	Asp	Gly	Thr	Met	Asp	Met	Val	Ile	355	360	365
Thr	Asp	Ala	Arg	Thr	Ser	Leu	Thr	Arg	Met	Ala	Pro	Ile	Leu	Leu	Gly	370	375	380
Leu	Asp	Lys	Gly	Ser	His	Val	Leu	Gln	Pro	Glu	Val	Leu	His	Ser	Lys	385	390	395

Ile Leu Ala Tyr Lys Ile Ile Pro Lys Leu Gly Asn Gly Leu Phe Ser
405 410 415
Val Asp Gly Glu Lys Phe Pro Leu Glu Pro Leu Gln Val Glu Ile Met
420 425 430
Pro Arg Leu Cys Lys Thr Leu Leu Arg Asn Gly Arg Tyr Val Asp Thr
435 440 445
Asp Phe Asp Ser Met
450

<210> 13
<211> 436
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 13
Leu Leu Ile Asp His Val Ser Arg Lys Ser Arg Ala Asn Thr Gly Glu
1 5 10 15
Glu Asn Ile Ser Ser Gly Thr Val Glu Glu Ile Leu Glu Lys Ser Tyr
20 25 30
Glu Asn Ser Lys Arg Asn Arg Ser Ile Leu Val Ile Ile Asn Pro His
35 40 45
Gly Gly Lys Gly Thr Ala Lys Asn Leu Phe Leu Thr Lys Ala Arg Pro
50 55 60
Ile Leu Val Glu Ser Gly Cys Lys Ile Glu Ile Ala Tyr Thr Lys Tyr
65 70 75 80
Ala Arg His Ala Ile Asp Ile Ala Lys Asp Leu Asp Ile Ser Lys Tyr
85 90 95
Asp Thr Ile Ala Cys Ala Ser Gly Asp Gly Ile Pro Tyr Glu Val Ile
100 105 110
Asn Gly Leu Tyr Arg Arg Pro Asp Arg Val Asp Ala Phe Asn Lys Leu
115 120 125
Ala Val Thr Gln Leu Pro Cys Gly Ser Gly Asn Ala Met Ser Ile Ser
130 135 140
Cys His Trp Thr Asn Asn Pro Ser Tyr Ala Ala Leu Cys Leu Val Lys
145 150 155 160
Ser Ile Glu Thr Arg Ile Asp Leu Met Cys Cys Ser Gln Pro Ser Tyr
165 170 175
Met Asn Glu Trp Pro Arg Leu Ser Phe Leu Ser Gln Thr Tyr Gly Val
180 185 190
Ile Ala Glu Ser Asp Ile Asn Thr Glu Phe Ile Arg Trp Met Gly Pro
195 200 205

Val Arg Phe Asn Leu Gly Val Ala Phe Asn Ile Ile Gln Gly Lys Lys
 210 215 220
 Tyr Pro Cys Glu Val Phe Val Lys Tyr Ala Ala Lys Ser Lys Lys Glu
 225 230 235 240
 Leu Lys Val His Phe Leu Glu Asn Lys Asp Lys Asn Lys Gly Cys Leu
 245 250 255
 Thr Phe Glu Pro Asn Pro Ser Pro Asn Ser Ser Pro Asp Leu Leu Ser
 260 265 270
 Lys Asn Asn Ile Asn Asn Ser Thr Lys Asp Glu Leu Ser Pro Asn Phe
 275 280 285
 Leu Asn Glu Asp Asn Phe Lys Leu Lys Tyr Pro Met Thr Glu Pro Val
 290 295 300
 Pro Arg Asp Trp Glu Lys Met Asp Ser Glu Leu Thr Asp Asn Leu Thr
 305 310 315 320
 Ile Phe Tyr Thr Gly Lys Met Pro Tyr Ile Ala Lys Asp Thr Lys Phe
 325 330 335
 Phe Pro Ala Ala Leu Pro Ala Asp Gly Thr Ile Asp Leu Val Ile Thr
 340 345 350
 Asp Ala Arg Ile Pro Val Thr Arg Met Thr Pro Ile Leu Leu Ser Leu
 355 360 365
 Asp Lys Gly Ser His Val Leu Glu Pro Glu Val Ile His Ser Lys Ile
 370 375 380
 Leu Ala Tyr Lys Ile Ile Pro Lys Val Glu Ser Gly Leu Phe Ser Val
 385 390 395 400
 Asp Gly Glu Lys Phe Pro Leu Glu Pro Leu Gln Val Glu Ile Met Pro
 405 410 415
 Met Leu Cys Lys Thr Leu Leu Arg Asn Gly Arg Tyr Ile Asp Thr Glu
 420 425 430
 Phe Glu Ser Met
 435

<210> 14
 <211> 380
 <212> PRT
 <213> Schizosaccharomyces pombe

<400> 14
 Cys Trp Val Asp Phe Val Glu Asn Ser Asp Gln Phe Cys Glu Tyr Leu
 1 5 10 15
 Leu Asp Val Ala Tyr Lys Gly Ile Lys Arg Ser Arg Arg Phe Ile Val
 20 25 30

Phe	Ile	Asn	Pro	His	Gly	Gly	Lys	Gly	Lys	Ala	Lys	His	Ile	Trp	Glu	35	40	45
Ser	Glu	Ala	Glu	Pro	Val	Phe	Ser	Ser	Ala	His	Ser	Ile	Cys	Glu	Val	50	55	60
Val	Leu	Thr	Arg	Arg	Lys	Asp	His	Ala	Lys	Ser	Ile	Ala	Lys	Asn	Leu	65	70	75
Asp	Val	Gly	Ser	Tyr	Asp	Gly	Ile	Leu	Ser	Val	Gly	Gly	Asp	Gly	Leu	85	90	95
Phe	His	Glu	Val	Ile	Asn	Gly	Leu	Gly	Glu	Arg	Asp	Asp	Tyr	Leu	Glu	100	105	110
Ala	Phe	Lys	Leu	Pro	Val	Cys	Met	Ile	Pro	Gly	Gly	Ser	Gly	Asn	Ala	115	120	125
Phe	Ser	Tyr	Asn	Ala	Thr	Gly	Gln	Leu	Lys	Pro	Ala	Leu	Thr	Ala	Leu	130	135	140
Glu	Ile	Leu	Lys	Gly	Arg	Pro	Thr	Ser	Phe	Asp	Leu	Met	Thr	Phe	Glu	145	150	155
Gln	Lys	Gly	Lys	Lys	Ala	Tyr	Ser	Phe	Leu	Thr	Ala	Asn	Tyr	Gly	Ile	165	170	175
Ile	Ala	Asp	Cys	Asp	Ile	Gly	Thr	Glu	Asn	Trp	Arg	Phe	Met	Gly	Glu	180	185	190
Asn	Arg	Ala	Tyr	Leu	Gly	Phe	Phe	Leu	Arg	Leu	Phe	Gln	Lys	Pro	Asp	195	200	205
Trp	Lys	Cys	Ser	Ile	Glu	Met	Asp	Val	Val	Ser	Ser	Asp	Arg	Thr	Glu	210	215	220
Ile	Lys	His	Met	Tyr	Glu	Lys	Ser	Lys	Asn	Leu	Ala	Pro	Met	Ser	Glu	225	230	235
Ser	Ser	Asp	Ser	Asp	Lys	Thr	Val	Ser	Thr	Ser	Pro	Glu	Ser	His	Leu	245	250	255
Leu	Thr	Phe	Glu	Ile	Asn	Asp	Leu	Ser	Ile	Phe	Cys	Ala	Gly	Leu	Leu	260	265	270
Pro	Tyr	Ile	Ala	Pro	Asp	Ala	Lys	Met	Phe	Pro	Ala	Ala	Ser	Asn	Asp	275	280	285
Asp	Gly	Leu	Ile	Asp	Val	Val	Ile	Val	Tyr	Ser	Lys	Gln	Phe	Arg	Lys	290	295	300
Ser	Leu	Leu	Ser	Met	Phe	Thr	Gln	Leu	Asp	Asn	Gly	Gly	Phe	Tyr	Tyr	305	310	315
Ser	Lys	His	Leu	Asn	Tyr	Tyr	Lys	Val	Arg	Ser	Phe	Arg	Phe	Thr	Pro	325	330	335

Val Asn Thr Gly Lys Arg His Tyr Phe Ala Leu Asp Gly Glu Ser Tyr
 340 345 350

Pro Leu Glu Pro Phe Glu Cys Arg Val Ala Pro Lys Leu Gly Thr Thr
 355 360 365

Leu Ser Pro Val Ala Gly Phe Gln Leu Leu Asp Ile
 370 375 380

<210> 15

<211> 415

<212> PRT

<213> Caenorhabditis elegans

<400> 15

Cys Arg Ser Asp Ala Glu Glu Asn Glu Gln Leu Thr Ser Val Ile Leu
 1 5 10 15

Ser Arg Lys Pro Pro Pro Gln Glu Gln Cys Arg Gly Asn Leu Leu Val
 20 25 30

Phe Ile Asn Pro Asn Ser Gly Thr Gly Lys Ser Leu Glu Thr Phe Ala
 35 40 45

Asn Thr Val Gly Pro Lys Leu Asp Lys Ser Leu Ile Arg Tyr Glu Val
 50 55 60

Val Val Thr Thr Gly Pro Asn His Ala Arg Asn Val Leu Met Thr Lys
 65 70 75 80

Ala Asp Leu Gly Lys Phe Asn Gly Val Leu Ile Leu Ser Gly Asp Gly
 85 90 95

Leu Val Phe Glu Ala Leu Asn Gly Ile Leu Cys Arg Glu Asp Ala Phe
 100 105 110

Arg Ile Phe Pro Thr Leu Pro Ile Gly Ile Val Pro Ser Gly Ser Gly
 115 120 125

Asn Gly Leu Leu Cys Ser Val Leu Ser Lys Tyr Gly Thr Lys Met Asn
 130 135 140

Glu Lys Ser Val Met Glu Arg Ala Leu Glu Ile Ala Thr Ser Pro Thr
 145 150 155 160

Ala Lys Ala Glu Ser Val Ala Leu Tyr Ser Val Lys Thr Asp Asn Gln
 165 170 175

Ser Tyr Ala Ser Phe Leu Ser Ile Gly Trp Gly Leu Met Ala Asp Ile
 180 185 190

Asp Ile Asp Ser Glu Lys Trp Arg Lys Ser Leu Gly His His Arg Phe
 195 200 205

Thr Val Met Gly Phe Ile Arg Ser Cys Asn Leu Arg Ser Tyr Lys Gly
 210 215 220

Arg	Leu	Thr	Tyr	Arg	Pro	Tyr	Lys	Pro	Lys	Gly	Phe	His	Pro	Ser	Ser	225	230	235	240
Asn	Val	Phe	Ser	Val	Tyr	Glu	Lys	Thr	Thr	Gln	Gln	Arg	Ile	Asp	Asp	245	250	255	
Ser	Lys	Val	Lys	Thr	Asn	Gly	Ser	Val	Ser	Asp	Ser	Glu	Glu	Glu	Thr	260	265	270	
Met	Glu	Thr	Lys	Phe	Gln	Asn	Trp	Thr	Leu	Pro	Asp	Ser	Asp	Glu	Thr	275	280	285	
Leu	Ala	Val	Gly	Ser	Ser	Asp	Leu	Glu	Glu	Thr	Val	Val	Ile	Glu	Asp	290	295	300	
Asn	Phe	Val	Asn	Ile	Tyr	Ala	Val	Thr	Leu	Ser	His	Ile	Ala	Ala	Asp	305	310	315	320
Gly	Pro	Phe	Ala	Pro	Ser	Ala	Lys	Leu	Glu	Asp	Asn	Arg	Ile	His	Leu	325	330	335	
Ser	Tyr	Ile	Leu	Trp	Lys	Asp	Ile	Gly	Thr	Arg	Val	Asn	Ile	Ala	Lys	340	345	350	
Tyr	Leu	Leu	Ala	Ile	Glu	His	Glu	Thr	His	Leu	Asp	Leu	Pro	Phe	Val	355	360	365	
Lys	His	Val	Glu	Val	Ser	Ser	Met	Lys	Leu	Glu	Val	Ile	Ser	Glu	Gly	370	375	380	
Ser	His	Val	Val	Leu	Asp	Gly	Glu	Val	Val	Asp	Thr	Lys	Thr	Ile	Glu	385	390	395	400
Val	Ala	Ser	Thr	Lys	Asn	His	Ile	Ser	Val	Phe	Ser	Ser	Thr	Ala		405	410	415	

<210> 16

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Illustrative motif

<400> 16

Asn Glu Gln Lys

1

<210> 17

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Illustrative motif

<400> 17

Asn His Gln Lys

1

<210> 18

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Illustrative motif

<400> 18

Asn Asp Glu Gln

1

<210> 19

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Illustrative motif

<400> 19

Gln His Arg Lys

1

<210> 20

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Illustrative motif

<400> 20

Met Ile Leu Val

1

<210> 21

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Illustrative motif

<400> 21

Met Ile Leu Phe

1

<210> 22

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Illustrative motif

<400> 22

Ser Thr Asn Lys

1

<210> 23

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Illustrative motif

<400> 23

Ser Thr Pro Ala

1

<210> 24

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Illustrative motif

<400> 24

Ser Gly Asn Asp

1

<210> 25

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Illustrative motif

<400> 25

Ser Asn Asp Glu Gln Lys
1 5

<210> 26

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Illustrative motif

<400> 26

Asn Asp Glu Gln His Lys
1 5

<210> 27

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Illustrative motif

<400> 27

Asn Glu Gln His Arg Lys
1 5

<210> 28

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Illustrative motif

<400> 28

Val Leu Ile Met
1

<210> 29

<211> 182

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: 80432911

<400> 29

Ala Gly Ala Pro Gly Ala Asp Ala Cys Ser Val Pro Val Ser Glu Ile
 1 5 10 15

Ile Ala Val Glu Glu Thr Asp Val His Gly Lys His Gln Gly Ser Gly
 20 25 30

Lys Trp Gln Lys Met Glu Lys Pro Tyr Ala Phe Thr Val His Cys Val
 35 40 45

Lys Arg Ala Arg Arg His Arg Trp Lys Trp Ala Gln Val Thr Phe Trp
 50 55 60

Cys Pro Glu Glu Gln Leu Cys His Leu Trp Leu Gln Thr Leu Arg Glu
 65 70 75 80

Met Leu Glu Lys Leu Thr Ser Arg Pro Lys His Leu Leu Val Phe Ile
 85 90 95

Asn Pro Phe Gly Gly Lys Gly Gln Gly Lys Arg Ile Tyr Glu Arg Lys
 100 105 110

Val Ala Pro Leu Phe Thr Leu Ala Ser Ile Thr Thr Asp Ile Ile Val
 115 120 125

Thr Glu His Ala Asn Gln Ala Lys Glu Thr Leu Tyr Glu Ile Asn Ile
 130 135 140

Asp Lys Tyr Asp Gly Ile Val Cys Val Gly Gly Asp Gly Met Phe Ser
 145 150 155 160

Glu Val Leu His Gly Leu Ile Gly Arg Thr Gln Arg Ser Ala Gly Val
 165 170 175

Asp Gln Asn His Pro Arg
 180